Amendments to the Specification

Please replace the paragraph beginning at page 20, line 23, with the following rewritten paragraph:

--Ion-exchange chromatography (a variation of adsorption chromatography) can also be used to isolate enzymes according to the present invention. In ion-exchange chromatography, a solid adsorbent is used that has charged groups chemically linked to an inert solid. An ionic charge on an enzyme molecule causes the molecule to attach to an oppositely charged group on the solid support. The enzyme is subsequently released from the support by passing a solution containing an ion gradient over the solid adsorbent. Examples of solid supports are DEAE-cellulose, ~~DEAE-Sephadex™~~ DEAE-SEPHADEX™, ~~DEAE-Bio-Gel™~~ DEAE-BIO-GEL™, ~~DEAE-Sepharose™~~ DEAE-SEPHAROSE™, ~~DEAE-Sephacryl™~~ DEAE-SEPHACRYL™, ~~DEAE-Trisacryl™~~ DEAE-TRISACRYL™, ~~Q-Sepharose™~~ Q-SEPHAROSE™, ecteola cellulose, QAE-cellulose, express ion exchanger Q, PEI-cellulose, and other polystyrene-based anion exchangers (most of these support materials are available from Pharmacia).--

Please replace the paragraph beginning at page 41, line 18, with the following rewritten paragraph:

--Library Construction and Screening: The cloned PCR products were used as a template to produce a radiolabeled PCR probe for library screening. Briefly, the PCR reactions were performed as previously described, except that only 100 μM dCTP was used and 0.825 uL α-^{32}P-dCTP (5 μCi) was added to the reactions (reduction of the dCTP concentration prior to addition of the radiolabeled nuclide reduces error due to base misincorporation). The radiolabeled PCR products were purified using the ~~Wizard™~~ WIZARD™ PCR Prep Kit (Promega) and scintillation counted to assess radioactivity.--

Please replace the paragraph beginning at page 41, line 26, with the following rewritten paragraph:

--A genomic library of *A. nidulans* (SM222) sequences was constructed by digesting genomic DNA with *Bam*HI and ligating the resulting fragments into the similarly digested lambda DNA vector EMPL-3. Concatemers of the ligated DNA were packaged using the ~~Gigapack™ II~~

GIGAPACK™ II (Stratagene, La Jolla, California) *in vitro* packaging system. Approximately 10^5 recombinant lambda plaques were immobilised on nylon membranes (~~Genescreen Plus™~~ GENESCREEN PLUS™, Dupont, Wilmington, Delaware) and hybridized with the radiolabeled PCR product generated from *A. nidulans*. Single hybridizing clones were selected and rescreened. Lambda DNA was isolated with the ~~Wizard™~~ WIZARD™ Lambda DNA Extraction Kit (Promega), digested with restriction enzymes, and subcloned into the pUC18 cloning vector.--

Please replace the paragraph beginning at page 42, line 5, with the following rewritten paragraph:

--DNA Preparation and Sequencing of *A. nidulans* α-1, 2-mannosidase 1A: Subclones, from the *A. nidulans* library, that contained the full-length α-1,2-mannosidase genes were identified by Southern analysis and sequenced. Initial manual sequencing of the α-mannosidase 1A gene was performed according to the dideoxynucleotide method using the T7 sequencing kit (Pharmacia). Initial sequence data were obtained with the universal priming sites, and with specific sequence primers (primer walking). Final sequence data were provided by subcloning the fragments using various restriction enzymes and sequencing with an ABI373 automated fluorescent sequencer (Applied Biosystems, Foster, California). Open reading frames were identified and aligned with known α-1,2-mannosidase sequences. The α-mannosidase 1B gene was sequenced by cloning restriction fragments of the positive lambda subclone into ~~BlueScript II™~~ BLUESCRIPT II™ cloning vector (Stratagene, La Jolla California) and sequencing on an ABI373 sequencer, using the universal priming sites of the vector.--

Please replace the paragraph beginning at page 42, line 31, with the following rewritten paragraph:

--Reverse-transcriptase PCR was performed using ~~Superscript II™~~ SUPERSCRIPT II™ reverse transcriptase (Gibco BRL) for first-strand cDNA synthesis using an oligo-dT primer followed by PCR amplification of the cDNA. The oligo-dT primer was annealed to the RNA by adding 1 μL of oligo-dT primer (500 μg/mL) to 5 μL of RNA (approx. 1-3 μg) and 6 μL of H_2O/DEPC. The mixture was heated to 70°C for 10 minutes and then quickly chilled on ice. Reverse transcription was achieved by addition of 4 μL "First Strand Buffer" (250 mM Tris-HCl pH 8.3, 375 mM KCl, 15 mM $MgCl_2$), 2 μL 0.1 M dithiothrectol (DTT), 1 μL 10 mM dNTPs, and 1 μL (200 U) ~~Superscript~~

H™ SUPERSCRIPT II™ reverse transcriptase, followed by incubation at 42°C for 50 minutes. After first-strand cDNA synthesis, the RNA was digested by the addition of 1 μL (2 U) RNAase H, and incubated at 37°C for 20 minutes. The cDNA was used to amplify regions containing putative introns for comparison with genomic DNA amplification.--